EXHIBIT A: MARKED VERSION SHOWING CHANGES MADE IN THE SPECIFICATION

U.S. APPLICATION SERIAL NO. 09/616,849

(ATTORNEY DOCKET NO. 9301-044)

(as amended February 5, 2002)

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EXHIBIT B: MARKED VERSION OF AMENDED CLAIMS
U.S. APPLICATION SERIAL NO. 09/616,849
(ATTORNEY DOCKET NO. 9301-044)

(as amended February 5, 2002)

1. (Amended) A method for evaluating [the] binding properties of a probe to a target molecule, said method comprising comparing the amount of binding of molecules in a first sample to the probe with the amount of binding of molecules in a second sample to the probe, wherein:

(a) the first sample comprises a plurality of molecules of the [same] target molecule; and

(b) the second sample comprises a plurality of different [target] molecules, wherein the first sample is at least 75% pure in said target molecule.

2. Canceled.

3. Canceled.

4. (Amended) The method of claim [2] 1 wherein the first sample is at least 90% pure in said target molecule.

5. (Amended) The method of claim [2] 4 wherein the first sample is at least 95% pure in said target molecule.

6. (Amended) The method of claim [2] 5 wherein the first sample is at least 99% pure in said target molecule.

7. (Amended) The method of claim 1 wherein each of said plurality of different [target molecule] molecules in the second sample is different from the [same] target [molecules] molecule in the first sample.

8. (Amended) The method of claim 1 wherein [the] a sensitivity of the probe is

determined, wherein said sensitivity is the absolute amount of molecules of said target molecule that bind to said probe.

9. (Amended) The method of claim 8 wherein the sensitivity of the probe is determined from the amount of binding of molecules of the [particular] target molecule in the first sample to the probe.

10. (Amended) The method of claim 1 wherein [the] a specificity of the probe is determined, wherein said specificity is the amount of molecules of said target molecule that bind to said probe relative to the amount of other molecules that bind to said probe under the same binding conditions.

11. (Amended) The method of claim 10 wherein the specificity of the probe is determined from [the] a ratio of the amount of binding to the probe of the [same] molecules of the target [molecules] molecule in the first sample [to the probe] to the amount of binding to the probe of molecules of the different [target] molecules in the second sample [to the probe].

12. (Amended) The method of claim 1 wherein the molecules of the [same] target molecule in the first sample are detectably labeled.

13. (Amended) The method of claim 1 wherein the molecules of the plurality of different [target] molecules in the second sample are detectably labeled.

15. (Amended) The method of claim 1 wherein:

(a) the molecules of the [same] target molecule in the first sample are detectably labeled with a first label; and

(b) the molecules of the plurality of different target molecules in the second sample are detectably labeled with a second label,

the first label being distinguishable from the second label.

20. (Amended) The method of claim 1 wherein the probe is a polynucleotide probe [having] comprising a [particular] predetermined nucleotide sequence.

22. (Amended) The method of claim 21 wherein the [particular] predetermined nucleotide sequence of the polynucleotide probe is complementary to at least a hybridizable portion of the nucleotide sequence of the polynucleotide molecules in the first sample.

23. (Amended) The method of claim 21 wherein the molecules of the different target molecules in the second sample are polynucleotide molecules [having a] comprising polynucleotide [sequence] sequences that [is] are different from the nucleotide sequence of the polynucleotide molecules in the first sample.

25. (Amended) The method of claim 20 wherein the polynucleotide probe is one of a plurality of polynucleotide probes [having] comprising different nucleotide sequences.

27. (Amended) A method for evaluating [the] binding properties of a polynucleotide probe [having] comprising a [particular] predetermined nucleotide sequence to a target [polynucleotide] nucleotide sequence, said method comprising comparing the amount of hybridization of polynucleotides in a first sample to the polynucleotide probe with the amount of hybridization of polynucleotides in a second sample to the polynucleotide probe, wherein:

(a) the first sample comprises a plurality of [the same target] polynucleotide molecules [having a] comprising said target nucleotide sequence; and

(b) the second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide molecule [has] comprises a sequence that is different from the nucleotide [sequence] sequences of any other polynucleotide molecules in said plurality of different polynucleotide molecules,

wherein the first sample is at least 75% pure in polynucleotide molecules comprising said target nucleotide sequence.

28. (Amended) The method of claim 27 wherein the [particular] predetermined

nucleotide sequence of the polynucleotide probe is complementary to at least a hybridizable portion of the target nucleotide sequence [of the target polynucleotide] in the first sample.

29. (Amended) The method of claim 27 wherein the target polynucleotide sequence in the first sample [corresponds to] is a nucleotide sequence of a gene or gene transcript of a cell or organism, or [to] of an mRNA, cDNA or cRNA derived therefrom.

30. (Amended) The method of claim 27 wherein the plurality of different polynucleotide molecules in the second sample [corresponds to] comprise nucleotide sequences of a plurality of [different] genes or gene transcripts of a cell or organism.

31. Canceled.

32. Canceled.

33. (Amended) The method of claim [31] 27 wherein the first sample is at least 90% pure in said polynucleotide molecules comprising said target nucleotide sequence.

34. (Amended) The method of claim [31] 33 wherein the first sample is at least 95% pure in said polynucleotide molecules comprising said target nucleotide sequence.

35. (Amended) The method of claim [31] 34 wherein in the first sample is at least 99% pure in said polynucleotide molecules comprising said target nucleotide sequence.

36. (Twice Amended) The method of claim [31] 27 wherein each different polynucleotide molecule in the second sample [has] does not comprise [a nucleotide sequence different from] the target nucleotide sequence.

37. (Amended) The method of claim 36 wherein:

(a) the target polynucleotide sequence in the first sample [corresponds to] is a sequence of a gene or gene transcript of a cell or organism; and

(b) the second sample comprises a polynucleotide sample from a deletion mutant of the cell or organism,

wherein the deletion mutant of the cell or organism does not express the gene or gene transcript [corresponding to the target polynucleotide in the first sample].

38. (Amended) The method of claim [31] 27 wherein the plurality of different polynucleotide molecules in the second sample comprises:

(a) polynucleotide molecules [having a nucleotide sequence that is the same as] comprising the target nucleotide sequence [in the first sample], and

(b) a plurality of different polynucleotide molecules, each [having] comprising a different nucleotide sequence [that is different from] and each not comprising the target nucleotide sequence.

39. (Twice Amended) The method of claim 38 wherein:

(a) the target [polynucleotide corresponds to] nucleotide sequence comprises a sequence of a gene or gene transcript of a cell or organism; and

(b) the second sample comprises a polynucleotide sample from a wild-type strain of the cell or organism,

wherein the wild-type strain of the cell or organism expresses the gene or gene transcript [corresponding to the target polynucleotide].

40. (Amended) The method of claim 27 wherein:

(a) the first sample further comprises polynucleotide molecules that do not [having a nucleotide sequence different from] comprise the target nucleotide sequence [of said same target polynucleotide]; and

(b) the second sample lacks said [same target] polynucleotide molecules comprising said target nucleotide sequence.

41. Canceled.

42. (Amended) The method of claim 41 wherein:

(a) the target [polynucleotide corresponds to] nucleotide sequence is a sequence of a gene or gene transcript of a cell or organism;

(b) the first sample comprises a polynucleotide sample from a wild-type strain of the cell or organism which expresses the gene or gene transcript [corresponding to the target polynucleotide]; and

(c) the second sample comprises a polynucleotide sample from a deletion mutant of the cell or organism which does not express the gene or gene transcript [corresponding to the target polynucleotide].

43. (Amended) The method of claim 27 wherein

(a) the first sample further comprises polynucleotide molecules [having a nucleotide sequence different from] that do not comprise the target nucleotide sequence [of said same target polynucleotide]; and

(b) the second sample comprises:

(i) polynucleotide molecules [having a nucleotide sequence that is the same as] comprising the target nucleotide sequence, and

(ii) a plurality of different polynucleotide molecules, each different polynucleotide molecule [having] comprising a different nucleotide sequence [that is different from] and not comprising the target nucleotide sequence,

wherein the amount of polynucleotide molecules in the first sample [having] comprising the target nucleotide sequence differs by at least a factor of two from the amount of polynucleotide molecules in the second sample [having] comprising the target nucleotide sequence.

55. (Amended) The method of claim 27 wherein [the] a sensitivity of the polynucleotide probe is determined, wherein said sensitivity is the absolute amount of said polynucleotide molecules comprising said target nucleotide sequence that bind to said polynucleotide probe.

56. (Amended) The method of claim 55 wherein the sensitivity of the polynucleotide

probe is determined from the amount of hybridization of [target] said polynucleotide molecules in the first sample to the polynucleotide probe.

57. (Amended) The method of claim 27 wherein [the] a specificity of the polynucleotide probe is determined, wherein said specificity is the amount of said polynucleotide molecules comprising said target nucleotide sequence that bind to said polynucleotide probe relative to the amount of polynucleotide molecules not comprising said target nucleotide sequence that bind to the probe under the same binding conditions.

58. (Amended) The method of claim 57 wherein the specificity of the polynucleotide probe is determined from [the] a ratio of the amount of hybridization of [target] polynucleotide molecules in the first sample to the polynucleotide probe to the amount of hybridization of polynucleotide molecules in the second sample to the polynucleotide probe.

59. (Amended) The method of claim 27 wherein the [target] polynucleotide molecules in the first sample are detectably labeled.

62. (Amended) The method of claim 27 wherein:

(a) the [target] polynucleotide molecules in the first sample are labeled with a first label; and

(b) the polynucleotide molecules in the second sample are labeled with a second label,

the first label being distinguishable from the second label.

67. (Amended) A method for evaluating [the] binding properties of a plurality of polynucleotide probes to a target [polynucleotide] nucleotide sequence wherein each polynucleotide probe in the plurality of polynucleotide probes [has] comprises a [particular] predetermined nucleotide sequence,

said method comprising comparing the amount of hybridization of polynucleotides in a first sample to each polynucleotide probe in the plurality of polynucleotide probes with the amount of hybridization of polynucleotides in a second sample to each polynucleotide probe

in the plurality of polynucleotide probes, wherein:

(a) the first sample comprises a plurality of [the same target] polynucleotide molecules [having a] comprising said target nucleotide sequence; and

(b) the second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide molecule [has] comprises a [different] nucleotide sequence that is different from nucleotide sequence of any other polynucleotide molecules in said plurality of different polynucleotide molecules,

wherein the first sample is at least 75% pure in polynucleotide molecules comprising said target nucleotide sequence.

68. (Amended) The method of claim 67 wherein the [particular] predetermined nucleotide sequence of each polynucleotide probe is complementary to at least a hybridizable portion of the target nucleotide sequence [of the target polynucleotide in the first sample].

69. (Amended) The method of claim 67 wherein [the] a sensitivity of each polynucleotide probe in the plurality of different polynucleotide probes is determined, wherein said sensitivity is the absolute amount of said polynucleotide molecules comprising said target nucleotide sequence that bind to said polynucleotide probe.

70. (Amended) The method of claim 69 wherein the sensitivity of each polynucleotide probe in the plurality of polynucleotide probes is determined from the amount of hybridization of the [same target] polynucleotide molecules comprising said target nucleotide sequence in the first sample to each polynucleotide probe in the plurality of polynucleotide probes.

71. (Amended) The method of claim [69] 67 wherein [the] a specificity of each polynucleotide probe in the plurality of different polynucleotide probes is determined, wherein said specificity is the amount of said polynucleotide molecules comprising said target nucleotide sequence that bind to said polynucleotide probe relative to the amount of polynucleotide molecules not comprising said target nucleotide sequence that bind to the

probe under the same binding conditions.

72. (Amended) The method of claim 71 wherein the specificity of each polynucleotide probe in the plurality of polynucleotide probes is determined from [the] a ratio of

(a) the amount of hybridization of the [same target] polynucleotide molecules comprising said target nucleotide sequence in the first sample to each polynucleotide probe to

(b) the amount of hybridization of the plurality of different polynucleotide molecules in the second sample to each polynucleotide probe.

75. (Amended) The method of claim 67 wherein the first sample comprises two or more different [target] polynucleotide molecules

wherein none of the [two or more] plurality of different [target] polynucleotide molecules hybridizes or cross-hybridizes to a probe that also hybridizes or cross-hybridizes to another one of the [two or more] plurality of different [target] polynucleotide molecules.

85. (Amended) The method of [any one of claims 81-84] claim 84 wherein the second sample lacks said [same target molecule or] polynucleotide molecules of [in] said first sample.